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NOV 26 2002

1453A-40-1.ST25.txt
SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Cooper, Jonathan A.

Howell, Brian W.

<120> ISOLATION AND EXPRESSION OF A DISABLED PROTEIN GENE MdaB1 AND METHODS

<130> 14538A-40-1

<140> US 09/486,293

<141> 2000-08-22

<150> PCT/US98/17384

<151> 1998-08-21

<150> US 60/056,473

B1 <151> 1997-08-21

<160> 34

<170> PatentIn version 3.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequencing primer that hybridizes to pVP16 vector

<400> 1

gcaagatctt agggatcgat tgg

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<210> 2

<213> Mus dunni

<223>

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aga gat ctc ttt caa ctc atc tat gag ctg aag caa aga gaa gaa ttg Arg Asp Leu Phe Gln Leu Ile Tyr Glu Leu Lys Gln Arg Glu Glu Leu 155 160 165 170	773
gaa aaa aag gca caa aag gat aag cag tgt gaa caa gct gtg tac cag Glu Lys Lys Ala Gln Lys Asp Lys Gln Cys Glu Gln Ala Val Tyr Gln 175 180 185	821
acc att ttg gaa gag gat gtg gaa gat ccc gtg tac cag tac att gtg Thr Ile Leu Glu Glu Asp Val Glu Asp Pro Val Tyr Gln Tyr Ile Val 190 195 200	869
ttt gag gct gga cat gag cca atc cgt gat cct gaa aca gaa gag aac Phe Glu Ala Gly His Glu Pro Ile Arg Asp Pro Glu Thr Glu Glu Asn 205 210 215	917
att tac cag gtt ccc acc agc caa aag aag gaa ggt gtt tat gat gtg Ile Tyr Gln Val Pro Thr Ser Gln Lys Lys Glu Gly Val Tyr Asp Val 220 225 230	965
cca aaa agt caa cct gta agt gct gtg acc caa tta gaa ctt ttt gga Pro Lys Ser Gln Pro Val Ser Ala Val Thr Gln Leu Glu Leu Phe Gly 235 240 245 250	1013
gac atg tcc acc cct cct gat ata acc tct ccc cct act cct gca acc Asp Met Ser Thr Pro Pro Asp Ile Thr Ser Pro Pro Thr Pro Ala Thr 255 260 265	1061
cca ggt gat gcc ttt ctc ccg tcg tcg tcc cag acg ctt ccg ggg agt Pro Gly Asp Ala Phe Leu Pro Ser Ser Ser Gln Thr Leu Pro Gly Ser 270 275 280	1109
gca gat gtg ttt ggc tct atg tct ttc ggc act gct gct gta ccc tca Ala Asp Val Phe Gly Ser Met Ser Phe Gly Thr Ala Ala Val Pro Ser 285 290 295	1157
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ccc ctt gtt caa cag cag atc gcc atg ggt gct cag cca ccc gtc gct Pro Leu Val Gln Gln Gln Ile Ala Met Gly Ala Gln Pro Pro Val Ala 315 320 325 330	1253
cag gtg ata cca gga gct cag ccc atc gca tgg ggc cag cca ggt ctc Gln Val Ile Pro Gly Ala Gln Pro Ile Ala Trp Gly Gln Pro Gly Leu 335 340 345	1301
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cca gcc gcc ttc atg ccc aca caa act gtt atg cct tta gca gcc gcc Pro Ala Ala Phe Met Pro Thr Gln Thr Val Met Pro Leu Ala Ala Ala 365 370 375	1397
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380

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 Asp Ser Ala Arg Ser Ser Pro Gln Ser Asp Lys Pro Arg Gln Lys Met
 395 400 405 410

ggg aag gag tct ttc aag gat ttc cag atg gtc cag cct cca ccc gta 1541
 Gly Lys Glu Ser Phe Lys Asp Phe Gln Met Val Gln Pro Pro Pro Val
 415 420 425

ccc tcc cgg aag cct gac cag ccc tcc ctg acc tgt acc tca gag gcc 1589
 Pro Ser Arg Lys Pro Asp Gln Pro Ser Leu Thr Cys Thr Ser Glu Ala
 430 435 440

ttc tcc agt tac ttc aac aaa gtc ggg gtg gca cag gat aca gag gac 1637
 Phe Ser Ser Tyr Phe Asn Lys Val Gly Val Ala Gln Asp Thr Asp Asp
 445 450 455

tgt gat gac ttt gac atc tcc caa ctg aac ttg acc cct gtg act tct 1685
 Cys Asp Asp Phe Asp Ile Ser Gln Leu Asn Leu Thr Pro Val Thr Ser
 460 465 470

acc aca cca tct acc aac tca cct cca acc cca gcc cct agg cag agc 1733
 Thr Thr Pro Ser Thr Asn Ser Pro Pro Thr Pro Ala Pro Arg Gln Ser
 475 480 485 490

tct cca tcc aaa tca tca gca tcc cac gtc agt gac ccg acc gca gat 1781
 Ser Pro Ser Lys Ser Ser Ala Ser His Val Ser Asp Pro Thr Ala Asp
 495 500 505

gac atc ttc gaa gaa ggc ttt gaa agt ccc agc aaa agt gaa gaa caa 1829
 Asp Ile Phe Glu Glu Gly Phe Glu Ser Pro Ser Lys Ser Glu Glu Gln
 510 515 520

gaa gca cct gat gga tca cag gcc tcc tcc acc agt gat cca ttt ggg 1877
 Glu Ala Pro Asp Gly Ser Gln Ala Ser Ser Thr Ser Asp Pro Phe Gly
 525 530 535

gag ccc agt ggt gag ccc agt ggt gat aat ata agt cca caa gac ggt 1925
 Glu Pro Ser Gly Glu Pro Ser Gly Asp Asn Ile Ser Pro Gln Asp Gly
 540 545 550

agc tag atagcgcagg tctgggagcc agagcctctc tatgcgaaaa tcaacagacc 1981
 Ser
 555

taagaaatag catcaatgcg agctcatggt ggggtgcttca cggatggcat gggaatctgc 2041

agtacaacag gctctcttgg gctctcacct cacttcatcc cacagaaaaa ctcacagtcg 2101

cccagtgaag ccacctgaag aaggaacaac atgggtttttg gcaaccaatg gcagatacct 2161

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aaaaaaaaa 2231

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<213> Mus dunni

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20 25 30

Lys Arg Phe Lys Gly Glu Gly Val Arg Tyr Lys Ala Lys Leu Ile Gly
35 40 45

Ile Asp Glu Val Ser Ala Ala Arg Gly Asp Lys Leu Cys Gln Asp Ser
50 55 60

Met Met Lys Leu Lys Gly Val Val Ala Gly Ala Arg Ser Lys Gly Glu
65 70 75 80

His Lys Gln Lys Ile Phe Leu Thr Ile Ser Phe Gly Gly Ile Lys Ile
85 90 95

Phe Asp Glu Lys Thr Gly Ala Leu Gln His His His Ala Val His Glu
100 105 110

Ile Ser Tyr Ile Ala Lys Asp Ile Thr Asp His Arg Ala Phe Gly Tyr
115 120 125

Val Cys Gly Lys Glu Gly Asn His Arg Phe Val Ala Ile Lys Thr Ala
130 135 140

Gln Ala Ala Glu Pro Val Ile Leu Asp Leu Arg Asp Leu Phe Gln Leu
145 150 155 160

Ile Tyr Glu Leu Lys Gln Arg Glu Glu Leu Glu Lys Lys Ala Gln Lys
165 170 175

Asp Lys Gln Cys Glu Gln Ala Val Tyr Gln Thr Ile Leu Glu Glu Asp
180 185 190

Val Glu Asp Pro Val Tyr Gln Tyr Ile Val Phe Glu Ala Gly His Glu
195 200 205

Pro Ile Arg Asp Pro Glu Thr Glu Glu Asn Ile Tyr Gln Val Pro Thr
210 215 220

Ser Gln Lys Lys Glu Gly Val Tyr Asp Val Pro Lys Ser Gln Pro Val
Page 5

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Asp	Ile	Thr	Ser 260	Pro	Pro	Thr	Pro	Ala 265	Thr	Pro	Gly	Asp	Ala 270	Phe	Leu
Pro	Ser	Ser 275	Ser	Gln	Thr	Leu	Pro 280	Gly	Ser	Ala	Asp	Val 285	Phe	Gly	Ser
Met	Ser 290	Phe	Gly	Thr	Ala	Ala 295	Val	Pro	Ser	Gly	Tyr 300	Val	Ala	Met	Gly
Ala 305	Val	Leu	Pro	Ser	Phe 310	Trp	Gly	Gln	Gln	Pro 315	Leu	Val	Gln	Gln	Gln 320
Ile	Ala	Met	Gly	Ala 325	Gln	Pro	Pro	Val	Ala 330	Gln	Val	Ile	Pro	Gly 335	Ala
Gln	Pro	Ile	Ala 340	Trp	Gly	Gln	Pro	Gly 345	Leu	Phe	Pro	Ala	Thr 350	Gln	Gln
Ala	Trp	Pro 355	Thr	Val	Ala	Gly	Gln 360	Phe	Pro	Pro	Ala	Ala 365	Phe	Met	Pro
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Thr 385	Pro	Leu	Ala	Thr	Val 390	Pro	Gly	Thr	Asn	Asp 395	Ser	Ala	Arg	Ser	Ser 400
Pro	Gln	Ser	Asp	Lys 405	Pro	Arg	Gln	Lys	Met 410	Gly	Lys	Glu	Ser	Phe 415	Lys
Asp	Phe	Gln	Met 420	Val	Gln	Pro	Pro	Pro 425	Val	Pro	Ser	Arg	Lys 430	Pro	Asp
Gln	Pro	Ser 435	Leu	Thr	Cys	Thr	Ser 440	Glu	Ala	Phe	Ser	Ser 445	Tyr	Phe	Asn
Lys 450	Val	Gly	Val	Ala	Gln	Asp 455	Thr	Asp	Asp	Cys	Asp 460	Asp	Phe	Asp	Ile
Ser 465	Gln	Leu	Asn	Leu	Thr 470	Pro	Val	Thr	Ser	Thr 475	Thr	Pro	Ser	Thr	Asn 480

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Ala Ser His Val Ser Asp Pro Thr Ala Asp Asp Ile Phe Glu Glu Gly
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Phe Glu Ser Pro Ser Lys Ser Glu Glu Gln Glu Ala Pro Asp Gly Ser
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gagccgagca ctccgccaga gtgaatgaca tgcacggtgt tgggtgtcct ttctgaagg	180
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Met Ser Thr Glu Thr Glu Leu Gln Val Ala	1 5 10
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Val Lys Thr Ser Ala Lys Lys Asp Ser Arg Lys Lys Gly Gln Asp Arg	15 20 25
agc gaa gcc act ttg ata aag agg ttt aaa ggc gaa ggg gtc cgg tac	389
Ser Glu Ala Thr Leu Ile Lys Arg Phe Lys Gly Glu Gly Val Arg Tyr	30 35 40
aaa gcc aag ctg att ggg att gat gaa gtg tcc gca gct cgg gga gac	437
Lys Ala Lys Leu Ile Gly Ile Asp Glu Val Ser Ala Ala Arg Gly Asp	

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ttt gag gct gga cat gag cca atc cgt gat cct gaa aca gaa gag aac Phe Glu Ala Gly His Glu Pro Ile Arg Asp Pro Glu Thr Glu Glu Asn 205 210 215			917
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Lys Arg Phe Lys Gly Glu Gly Val Arg Tyr Lys Ala Lys Leu Ile Gly
 35 40 45

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Ile Asp Glu Val Ser Ala Ala Arg Gly Asp Lys Leu Cys Gln Asp Ser
50 55 60

Met Met Lys Leu Lys Gly Val Val Ala Gly Ala Arg Ser Lys Gly Glu
65 70 75 80

His Lys Gln Lys Ile Phe Leu Thr Ile Ser Phe Gly Gly Ile Lys Ile
85 90 95

Phe Asp Glu Lys Thr Gly Ala Leu Gln His His His Ala Val His Glu
100 105 110

Ile Ser Tyr Ile Ala Lys Asp Ile Thr Asp His Arg Ala Phe Gly Tyr
115 120 125

Val Cys Gly Lys Glu Gly Asn His Arg Phe Val Ala Ile Lys Thr Ala
130 135 140

Q\ Gln Ala Ala Glu Pro Val Ile Leu Asp Leu Arg Asp Leu Phe Gln Leu
145 150 155 160

Ile Tyr Glu Leu Lys Gln Arg Glu Glu Leu Glu Lys Lys Ala Gln Lys
165 170 175

Asp Lys Gln Cys Glu Gln Ala Val Tyr Gln Thr Ile Leu Glu Glu Asp
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Pro Ile Arg Asp Pro Glu Thr Glu Glu Asn
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Lys Arg Phe Lys Gly Glu Gly Val Arg Tyr Lys Ala Lys Leu Ile Gly
 35 40 45

Ile Asp Glu Val Ser Ala Ala Arg Gly Asp Lys Leu Cys Gln Asp Ser
 50 55 60

Met Met Lys Leu Lys Gly Val Val Ala Gly Ala Arg Ser Lys Gly Glu
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His Lys Gln Lys Ile Phe Leu Thr Ile Ser Phe Gly Gly Ile Lys Ile
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Phe Asp Glu Lys Thr Gly Ala Leu Gln His His His Ala Val His Glu
 100 105 110

Ile Ser Tyr Ile Ala Lys Asp Ile Thr Asp His Arg Ala Phe Gly Tyr
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Val Cys Gly Lys Glu Gly Asn His Arg Phe Val Ala Ile Lys Thr Ala
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Gln Ala Ala Glu Pro Val Ile Leu Asp Leu Arg Asp Leu Phe Gln Leu
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Ile Tyr Glu Leu Lys Gln Arg Glu Glu Leu Glu Lys Lys Ala Gln Lys
165 170 175

Asp Lys Gln Cys Glu Gln Ala Val Tyr Gln Thr Ile Leu Glu Glu Asp
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ccg aac agg aac ctg tca atg gac ttt gat gag ctt ctc gag gca acc 96
Pro Asn Arg Asn Leu Ser Met Asp Phe Asp Glu Leu Leu Glu Ala Thr
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aag 99
Lys

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Lys

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27

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1 5 10 15

Ser Arg Lys Lys
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<213> Mus dunni

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Ser

<210> 16

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<212> DNA

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<210> 18

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27

<210> 19

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<212> DNA

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<223> X = Any amino acid

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<212> PRT

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Tyr Gln Tyr Ile
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<210> 22

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<400> 22

Tyr Ile Tyr Val

1

<210> 23

<211> 30

<212> DNA

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<223> oligonucleotide for site directed mutagenesis

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cacaatgaac tggaagacgg gatcttcac

30

<210> 24

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<212> DNA

<213> Artificial sequence

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<223> oligonucleotide P2 for PCR genotyping

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24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide P2 for PCR genotyping

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24

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<211> 25

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<223> Oligonucleotide P3 for PCR genotyping

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25

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<220>

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<222> (8)..(9)

<223> X = Any amino acid

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<223> X = Any amino acid

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Gly Tyr Glu Asn Pro Thr Tyr Xaa Xaa Glu Xaa Xaa Xaa Xaa
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<210> 28

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<212> PRT

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Asn Phe Thr Asn Pro Val Tyr
1 5

<210> 29

<211> 7

<212> PRT

<213> NPXY motif of LDL receptor related protein

<400> 29

Asn Phe Asp Asn Pro Val Tyr
1 5

<210> 30

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<212> PRT

<213> Artificial Sequence

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<223> NPXY motif in peptides derived from p150 ship

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<223> NPXY motif in peptides derived from p150 ship

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<223> NPXY motif in peptides derived from insulin receptor

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